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RAW SEQUENCE LISTING

DATE: 05/16/2002

PATENT APPLICATION: US/09/718,803A

TIME: 17:12:27

Input Set : A:\99-62 SEQ.txt

Output Set: N:\CRF3\05162002\I718803A.raw

```

3 <110> APPLICANT: SHEPPARD, PAUL O.
4 JASPERS, STEPHEN R.
5 DEISHER, THERESA A.
6 BISHOP, PAUL D.
8 <120> TITLE OF INVENTION: METHOD OF FORMING A PEPTIDE-RECEPTOR
9 COMPLEX WITH ZSIG33
11 <130> FILE REFERENCE: 99-62
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/718,803A
C--> 13 <141> CURRENT FILING DATE: 2002-05-07
13 <150> PRIOR APPLICATION NUMBER: 60/166,765
14 <151> PRIOR FILING DATE: 1999-11-22
16 <160> NUMBER OF SEQ ID NOS: 16
18 <170> SOFTWARE: FastSEQ for Windows Version 3.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 351
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (1)...(351)
29 <400> SEQUENCE: 1
30 atg ccc tcc cca ggg acc gtc tgc agc ctc ctg ctc ctc ggc atg ctc      48
31 Met Pro Ser Pro Gly Thr Val Cys Ser Leu Leu Leu Leu Gly Met Leu
32 1 5 10 15
34 tgg ctg gac ttg gcc atg gca ggc tcc agc ttc ctg agc cct gaa cac      96
35 Trp Leu Asp Leu Ala Met Ala Gly Ser Ser Phe Leu Ser Pro Glu His
36 20 25 30
38 cag aga gtc cag cag aga aag gag tgc aag aag cca cca gcc aag ctg      144
39 Gln Arg Val Gln Gln Arg Lys Glu Ser Lys Lys Pro Pro Ala Lys Leu
40 35 40 45
41 cag ccc cga gct cta gca ggc tgg ctc cgc ccg gaa gat gga ggt caa      192
42 Gln Pro Arg Ala Leu Ala Gly Trp Leu Arg Pro Glu Asp Gly Gly Gln
43 50 55 60
45 gca gaa ggg gca gag gat gaa ctg gaa gtc cgg ttc aac gcc ccc ttt      240
46 Ala Glu Gly Ala Glu Asp Glu Leu Glu Val Arg Phe Asn Ala Pro Phe
47 65 70 75 80
49 gat gtt gga atc aag ctg tca ggg gtt cag tac cag cag cac agc cag      288
50 Asp Val Gly Ile Lys Leu Ser Gly Val Gln Tyr Gln Gln His Ser Gln
51 85 90 95
53 gcc ctg ggg aag ttt ctt cag gac atc ctc tgg gaa gag gcc aaa gag      336
54 Ala Leu Gly Lys Phe Leu Gln Asp Ile Leu Trp Glu Glu Ala Lys Glu
55 100 105 110
57 gcc cca gcc gac aag      351

```

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```

58 Ala Pro Ala Asp Lys
59      115
61 <210> SEQ ID NO: 2
62 <211> LENGTH: 117
63 <212> TYPE: PRT
64 <213> ORGANISM: Homo sapiens
66 <400> SEQUENCE: 2
67 Met Pro Ser Pro Gly Thr Val Cys Ser Leu Leu Leu Leu Gly Met Leu
68   1          5          10          15
69 Trp Leu Asp Leu Ala Met Ala Gly Ser Ser Phe Leu Ser Pro Glu His
70      20          25          30
71 Gln Arg Val Gln Gln Arg Lys Glu Ser Lys Lys Pro Pro Ala Lys Leu
72      35          40          45
73 Gln Pro Arg Ala Leu Ala Gly Trp Leu Arg Pro Glu Asp Gly Gly Gln
74      50          55          60
75 Ala Glu Gly Ala Glu Asp Glu Leu Glu Val Arg Phe Asn Ala Pro Phe
76      65          70          75          80
77 Asp Val Gly Ile Lys Leu Ser Gly Val Gln Tyr Gln Gln His Ser Gln
78      85          90          95
79 Ala Leu Gly Lys Phe Leu Gln Asp Ile Leu Trp Glu Glu Ala Lys Glu
80      100         105         110
81 Ala Pro Ala Asp Lys
82      115
84 <210> SEQ ID NO: 3
85 <211> LENGTH: 351
86 <212> TYPE: DNA
87 <213> ORGANISM: Artificial Sequence
89 <220> FEATURE:
90 <223> OTHER INFORMATION: Degenerate polynucleotide
W--> 92 <221> NAME/KEY: misc_feature
93 <222> LOCATION: (1)...(351)
94 <223> OTHER INFORMATION: n = A,T,C or G
W--> 96 <400> 3
W--> 97 atgccnwsnc cnggnacngt ntgywsnytn ytntyntng gnatgytntg gytn gayytn      60
W--> 98 gcnatggcng gnwsnwsntt yytnwsnccn garcaycarm gngtnarca rmgnaargar      120
W--> 99 wsnaaraarc cncngcnaa rytncarcen mgngcnytn gngntggyt nmgnccngar      180
W--> 100 gayggnggnc argcngargg ngcngargay garytngarg tnmgnttyaa ygcncntty      240
W--> 101 gaygtnggna thaarytnws nggngtnear taycarc arc aywsncargc nytnngnaar      300
W--> 102 ttyytncarg ayathytn g gargargcn aargargcnc cngcngayaa r      351
104 <210> SEQ ID NO: 4
105 <211> LENGTH: 1101
106 <212> TYPE: DNA
107 <213> ORGANISM: Homo sapiens
109 <220> FEATURE:
110 <221> NAME/KEY: CDS
111 <222> LOCATION: (1)...(1101)
113 <400> SEQUENCE: 4
114 atg tgg aac gcg acg ccc agc gaa gag ccg ggg ttc aac ctc aca ctg      48
115 Met Trp Asn Ala Thr Pro Ser Glu Glu Pro Gly Phe Asn Leu Thr Leu

```

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116	1	5	10	15	
118	gcc gac ctg gac tgg gat gct tcc ccc ggc aac gac tcg ctg ggc gac	96			
119	Ala Asp Leu Asp Trp Asp Ala Ser Pro Gly Asn Asp Ser Leu Gly Asp				
120	20 25 30				
121	gag ctg ctg cag ctc ttc ccc gcg ccg ctg ctg gcg ggc gtc aca gcc	144			
122	Glu Leu Leu Gln Leu Phe Pro Ala Pro Leu Leu Ala Gly Val Thr Ala				
123	35 40 45				
125	acc tgc gtg gca ctc ttc gtg gtg ggt atc gct ggc aac ctg ctc acc	192			
126	Thr Cys Val Ala Leu Phe Val Val Gly Ile Ala Gly Asn Leu Leu Thr				
127	50 55 60				
129	atg ctg gtg gtg tcg cgc ttc cgc gag ctg cgc acc acc acc aac ctc	240			
130	Met Leu Val Val Ser Arg Phe Arg Glu Leu Arg Thr Thr Thr Asn Leu				
131	65 70 75 80				
133	tac ctg tcc agc atg gcc ttc tcc gat ctg ctc atc ttc ctc tgc atg	288			
134	Tyr Leu Ser Ser Met Ala Phe Ser Asp Leu Leu Ile Phe Leu Cys Met				
135	85 90 95				
137	ccc ctg gac ctc gtt cgc ctc tgg cag tac cgg ccc tgg aac ttc ggc	336			
138	Pro Leu Asp Leu Val Arg Leu Trp Gln Tyr Arg Pro Trp Asn Phe Gly				
139	100 105 110				
141	gac ctc ctc tgc aaa ctc ttc caa ttc gtc agt gag agc tgc acc tac	384			
142	Asp Leu Leu Cys Lys Leu Phe Gln Phe Val Ser Glu Ser Cys Thr Tyr				
143	115 120 125				
145	gcc acg gtg ctc acc atc aca gcg ctg agc gtc gag cgc tac ttc gcc	432			
146	Ala Thr Val Leu Thr Ile Thr Ala Leu Ser Val Glu Arg Tyr Phe Ala				
147	130 135 140				
149	atc tgc ttc cca ctc cgg gcc aag gtg gtg gtc acc aag ggg cgg gtg	480			
150	Ile Cys Phe Pro Leu Arg Ala Lys Val Val Val Thr Lys Gly Arg Val				
151	145 150 155 160				
153	aag ctg gtc atc ttc gtc atc tgg gcc gtg gcc ttc tgc agc gcc ggg	528			
154	Lys Leu Val Ile Phe Val Ile Trp Ala Val Ala Phe Cys Ser Ala Gly				
155	165 170 175				
157	ccc atc ttc gtg cta gtc ggg gtg gag cac gag aac ggc acc gac cct	576			
158	Pro Ile Phe Val Leu Val Gly Val Glu His Glu Asn Gly Thr Asp Pro				
159	180 185 190				
161	tgg gac acc aac gag tgc cgc ccc acc gag ttt gcg gtg cgc tct gga	624			
162	Trp Asp Thr Asn Glu Cys Arg Pro Thr Glu Phe Ala Val Arg Ser Gly				
163	195 200 205				
165	ctg ctc acg gtc atg gtg tgg gtg tcc agc atc ttc ttc ttc ctt cct	672			
166	Leu Leu Thr Val Met Val Trp Val Ser Ser Ile Phe Phe Phe Leu Pro				
167	210 215 220				
169	gtc ttc tgt ctc acg gtc ctc tac agt ctc atc ggc agg aag ctg tgg	720			
170	Val Phe Cys Leu Thr Val Leu Tyr Ser Leu Ile Gly Arg Lys Leu Trp				
171	225 230 235 240				
173	cgg agg agg cgc ggc gat gct gtc gtg ggt gcc tcg ctc agg gac cag	768			
174	Arg Arg Arg Arg Gly Asp Ala Val Val Gly Ala Ser Leu Arg Asp Gln				
175	245 250 255				
177	aac cac aag caa acc gtg aaa atg ctg gct gta gtg gtg ttt gcc ttc	816			
178	Asn His Lys Gln Thr Val Lys Met Leu Ala Val Val Val Phe Ala Phe				
179	260 265 270				

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```

181 atc ctc tgc tgg ctc ccc ttc cac gta ggg cga tat tta ttt tcc aaa      864
182 ile leu cys trp leu pro phe his val gly arg tyr leu phe ser lys
183      275      280      285
185 tcc ttt gag cct ggc tcc ttg gag att gct cag atc agc cag tac tgc      912
186 ser phe glu pro gly ser leu glu ile ala gln ile ser gln tyr cys
187      290      295      300
189 aac ctc gtg tcc ttt gtc ctc ttc tac ctc agt gct gcc atc aac ccc      960
190 asn leu val ser phe val leu phe tyr leu ser ala ala ile asn pro
191      305      310      315      320
193 att ctg tac aac atc atg tcc aag aag tac cgg gtg gca gtg ttc aga      1008
194 ile leu tyr asn ile met ser lys lys tyr arg val ala val phe arg
195      325      330      335
197 ctt ctg gga ttc gaa ccc ttc tcc cag aga aag ctc tcc act ctg aaa      1056
198 leu leu gly phe glu pro phe ser gln arg lys leu ser thr leu lys
199      340      345      350
201 gat gaa agt tct cgg gcc tgg aca gaa tct agt att aat aca tga      1101
202 asp glu ser ser arg ala trp thr glu ser ser ile asn thr *
203      355      360      365
205 <210> SEQ ID NO: 5
206 <211> LENGTH: 366
207 <212> TYPE: PRT
208 <213> ORGANISM: Homo sapiens
210 <400> SEQUENCE: 5
211 Met Trp Asn Ala Thr Pro Ser Glu Glu Pro Gly Phe Asn Leu Thr Leu
212 1 5 10 15
213 Ala Asp Leu Asp Trp Asp Ala Ser Pro Gly Asn Asp Ser Leu Gly Asp
214 20 25 30
215 Glu Leu Leu Gln Leu Phe Pro Ala Pro Leu Leu Ala Gly Val Thr Ala
216 35 40 45
217 Thr Cys Val Ala Leu Phe Val Val Gly Ile Ala Gly Asn Leu Leu Thr
218 50 55 60
219 Met Leu Val Val Ser Arg Phe Arg Glu Leu Arg Thr Thr Thr Asn Leu
220 65 70 75 80
221 Tyr Leu Ser Ser Met Ala Phe Ser Asp Leu Leu Ile Phe Leu Cys Met
222 85 90 95
223 Pro Leu Asp Leu Val Arg Leu Trp Gln Tyr Arg Pro Trp Asn Phe Gly
224 100 105 110
225 Asp Leu Leu Cys Lys Leu Phe Gln Phe Val Ser Glu Ser Cys Thr Tyr
226 115 120 125
227 Ala Thr Val Leu Thr Ile Thr Ala Leu Ser Val Glu Arg Tyr Phe Ala
228 130 135 140
229 Ile Cys Phe Pro Leu Arg Ala Lys Val Val Val Thr Lys Gly Arg Val
230 145 150 155 160
231 Lys Leu Val Ile Phe Val Ile Trp Ala Val Ala Phe Cys Ser Ala Gly
232 165 170 175
233 Pro Ile Phe Val Leu Val Gly Val Glu His Glu Asn Gly Thr Asp Pro
234 180 185 190
235 Trp Asp Thr Asn Glu Cys Arg Pro Thr Glu Phe Ala Val Arg Ser Gly
236 195 200 205

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```

237 Leu Leu Thr Val Met Val Trp Val Ser Ser Ile Phe Phe Phe Leu Pro
238      210                      215                      220
239 Val Phe Cys Leu Thr Val Leu Tyr Ser Leu Ile Gly Arg Lys Leu Trp
240      225                      230                      235                      240
241 Arg Arg Arg Arg Gly Asp Ala Val Val Gly Ala Ser Leu Arg Asp Gln
242      245                      250                      255
243 Asn His Lys Gln Thr Val Lys Met Leu Ala Val Val Val Phe Ala Phe
244      260                      265                      270
245 Ile Leu Cys Trp Leu Pro Phe His Val Gly Arg Tyr Leu Phe Ser Lys
246      275                      280                      285
247 Ser Phe Glu Pro Gly Ser Leu Glu Ile Ala Gln Ile Ser Gln Tyr Cys
248      290                      295                      300
249 Asn Leu Val Ser Phe Val Leu Phe Tyr Leu Ser Ala Ala Ile Asn Pro
250      305                      310                      315                      320
251 Ile Leu Tyr Asn Ile Met Ser Lys Lys Tyr Arg Val Ala Val Phe Arg
252      325                      330                      335
253 Leu Leu Gly Phe Glu Pro Phe Ser Gln Arg Lys Leu Ser Thr Leu Lys
254      340                      345                      350
255 Asp Glu Ser Ser Arg Ala Trp Thr Glu Ser Ser Ile Asn Thr
256      355                      360                      365
258 <210> SEQ ID NO: 6
259 <211> LENGTH: 1098
260 <212> TYPE: DNA
261 <213> ORGANISM: Artificial Sequence
263 <220> FEATURE:
264 <223> OTHER INFORMATION: degenerate sequence
W--> 266 <221> NAME/KEY: misc_feature
267 <222> LOCATION: (1)...(1098)
268 <223> OTHER INFORMATION: n = A,T,C or G
W--> 270 <400> 6
W--> 271 atgtggaayg cnacnccnws ngargarccn ggnttyaayy tnacnytngc ngayytngay      60
W--> 272 tgggagycnw snccnggnaa ygaywsnytn ggngaygary tnytn Caryt nttyccngcn      120
W--> 273 ccnytnytng cnggngtnac ngcnacntgy gtngcnytn tngtngtngg nathgcnngn      180
W--> 274 aayytnytna cnatgytngt ngtnwsnmgn ttymngary tnmgnacnac nacnaayytn      240
W--> 275 tayytnwsnw snatggcntt ywsngayytn ytnathhtty tntgyatgcc nytngayytn      300
W--> 276 gtnmgnytn ggcartaymg nccntggaay ttyggngayy tnytn tgyaa rytnttycar      360
W--> 277 ttygtwnsng arwsntgyac ntaygcnacn gtnytnacna thacngcnyt nwsngtngar      420
W--> 278 mgntayttyg cnathtgytt yccnytnmgn gcnaargtng tngtnacnaa rggnmngntn      480
W--> 279 aarytngtna thttgytnat htgggcngtn gcnttytgyw sngcnggncc nathttygtn      540
W--> 280 ytngtngngng tngarcayga raayggnacn gayccntggg ayacnaayga rtgymgnccn      600
W--> 281 acngarttyg cngtnmgnws nggnytnytn acngtnatgg tntgggtngws nwsnathhty      660
W--> 282 ttyttyytnc cngtnttytg yytnacngtn ytnaywsny tnathggngm naarytn tgg      720
W--> 283 mgnmgnmgnm gngngaygc ngtngtnggn gcnwsnytnm gngaycaraa ycayaarcar      780
W--> 284 acngtnaara tgytngcngt ngtngtntty gcnttyathy tntgytgyt nccnttycay      840
W--> 285 gtnggnmgnt ayynttyws naarwsntty garccnggnw snytn garat hgncarath      900
W--> 286 wsncartayt gyaayytngt nwsnttygtn ytnttytay twnsngcngc nathaayccn      960
W--> 287 athytntaya ayathatgws naaraartay mgngtngcng tnttymgnyt nytnngntty      1020
W--> 288 garccnttyw sncarmgnaa rytnwsnacn ytnaargay arwsnwsnmg ngcntggacn      1080
W--> 289 garwsnwsna thaayacn                                     1098

```

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 6,9,12,15,18,21,27,30,33,36,39,42,48,54,60,63,69,72,75,78,84
Seq#:3; N Pos. 87,90,102,105,114,123,132,135,138,144,150,153,156,159,162
Seq#:3; N Pos. 165,171,174,177,186,189,195,201,204,216,222,225,234,237,246
Seq#:3; N Pos. 249,258,261,264,267,285,291,294,297,306,318,330,339,342,345
Seq#:6; N Pos. 12,15,18,21,30,33,42,45,48,51,57,69,72,75,78,87,90,93,102
Seq#:6; N Pos. 105,111,117,120,123,126,129,132,135,138,141,144,147,153,156
Seq#:6; N Pos. 159,165,168,171,177,180,186,189,192,198,201,204,207,210,216
Seq#:6; N Pos. 222,225,228,231,234,240,246,249,252,258,264,270,273,282,291
Seq#:6; N Pos. 294,300,303,306,309,321,324,336,342,345,354,366,369,375,381
Seq#:6; N Pos. 387,390,393,396,399,405,408,411,414,417,423,432,444,447,450
Seq#:6; N Pos. 453,459,462,465,468,474,477,480,486,489,498,507,510,513,522
Seq#:6; N Pos. 525,528,531,540,543,546,549,552,567,570,576,585,597,600,603
Seq#:6; N Pos. 612,615,618,621,624,627,630,633,636,642,648,651,654,669,672
Seq#:6; N Pos. 675,684,687,690,693,699,702,708,711,717,723,726,729,732,735
Seq#:6; N Pos. 741,744,747,750,753,756,759,762,783,786,795,798,801,804,807
Seq#:6; N Pos. 813,822,831,834,843,846,849,855,861,867,876,879,882,885,894
Seq#:6; N Pos. 903,918,921,924,930,933,942,945,948,951,960,966,981,993,996
Seq#:6; N Pos. 999,1002,1008,1011,1014,1017,1026,1032,1038,1044,1047,1050
Seq#:6; N Pos. 1053,1065,1068,1071,1074,1080,1086,1089,1098

VERIFICATION SUMMARY

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Input Set : A:\99-62 SEQ.txt

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:92 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:96 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3
L:97 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:98 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:60
L:99 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:120
L:100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:180
L:101 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:240
L:102 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:300
L:266 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:270 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
L:271 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:60
L:273 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:120
L:274 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:180
L:275 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:240
L:276 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:300
L:277 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:360
L:278 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:420
L:279 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:480
L:280 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:540
L:281 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:600
L:282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:660
L:283 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:720
L:284 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:780
L:285 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:840
L:286 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:900
L:287 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:960
L:288 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:1020
L:289 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:1080
L:481 M:283 W: Missing Blank Line separator, <400> field identifier